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HUMAN EPIGENETICS

# Showing your age

Characterizing the molecular features of ageing is key for understanding the mechanisms of normal and premature ageing, and has applications such as predicting the age of an individual from a forensic sample. A new study has characterized the DNA methylomes of large cohorts of humans, identifying various predictors of age and ageing rates.

Hannum *et al.* carried out microarray-based genome-wide DNA methylation analysis of the blood of 482 individuals ranging from ages 19 to 101. They found 71 sites for which the methylation status was highly correlated with age, allowing age prediction on the basis of this methylation signature. Prediction was accurate to within ~5 years, both in this cohort and in an independent cohort of 174 individuals. Furthermore, most of the markers were located near to genes linked to ageing-related processes and diseases.

Corbis

These blood-derived signatures were also applicable to various other normal tissues, implying that molecular ageing at the level of DNA methylation is similar across tissue types.

The authors calculated apparent methylomic ageing rates (AMARs), which is the ratio of the methylation-derived molecular age to the actual chronological age, and looked for determinants of this ageing rate. As expected, males tended to age faster than females. Also, exome sequencing of a subset of the cohort identified three genetic variants that influence the ageing rate, seemingly by altering the methylation state of nearby age-dependent methylation sites.

It will be interesting to dissect the functional relevance of these methylation changes to ageing, including whether they are causes, or rather reporters, of the ageing process.

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**ORIGINAL RESEARCH PAPER** Hannum, G. *et al.* Genome-wide methylation profiles reveal quantitative views of human aging rates. *Mol. Cell* 21 Nov 2012 (doi:10.1016/j.molcel.2012.10.016)